International Journal of Agricultural Science and Research (IJASR)
ISSN(P): 2250-0057; ISSN(E): 2321-0087
Vol. 6, Issue 1, Feb 2016, 79-86

TRANS STELLAR
•Journal Publications •Research Consultancy

ASSESSMENTS OF GENETIC DIVERGENCE IN RECOMBINANT INBRED LINES FROM CROSS OF *G. HIRSUTUM* X *G. BARBADENSE* COTTON

YALLAPPA HARIJAN[1], NISHANTH G K[2], PAVITHRA K P[3], I S KATAGERI[4] & B M KHADI[5]

[1]*Ph.D Scholar, Dept. of Genetics and Plant Breeding, UAS, GKVK, Bangalore, Karnataka, India*

[2]*Ph.D Scholar, Dept. of Genetics and Plant Breeding, UAHS, Shimoga, Karnataka, India*

[3]*Senior Research Associate Maize R&D, JK Agri Genetics Ltd. Bangalore, Karnataka, India*

[4]*Professor and Head, Dept. of Agricultural Biotechnology, UAS, Dharwad, Karnataka, India*

[5]*Director of Education, UAS,Dharwad, Karnataka, India*

ABSTRACT

Genetic diversity in 190 derivatives of F9 generation of cross between G. hirsutum var. DS-28 and G. barbadense var. SBYF-425 assessed using Mahalanobis D^2 statistics, indicated presence of considerable diversity. The genotypes were grouped into three clusters based on plant morphological, yield and yield contributing characters and 85 genotypes formed ten clusters based on fibre quality traits. The contribution of various characters towards the expression of genetic divergence indicated that seed cotton yield per ha (kg) contributed highest (92.19 %) followed by plant height (6.81%) and ginning outturn (0.71%) whereas, among the 85 recombinant inbred lines 2.5% span length contributed to 45.85 % followed by uniformity ratio (42.44%) and fibre strength (11.29%) based on fibre quality traits.

KEYWORDS: Cotton, Genetic Diversity, Recombinant Inbred Lines, D^2 Analysis, Fibre

Received: Aug 07, 2015; **Accepted:** Dec 09, 2015; **Published:** Jan 08, 2016; **Paper Id.:** IJASRFEB201611

Original Article

INTRODUCTION

Cotton (Gossypium spp.) popularly known as “the white gold”, is an important commercial fibre crop grown under diverse agro climatic conditions around the world. It provides fibre, an important raw material for textile industry. In India, cotton provides means of livelihood to millions of farmers and workers and sustains cotton textile industry which annually produces cloth of the value exceeding a thousand crore rupees. Cotton seed had also gained the additional economic importance as a major contributor to edible oil, protein and other byproducts. The valuable biomass from cotton stalks has become very useful raw material for manufacture of particle boards, paper and other stationaries. In total, cotton has become a highly agro-industrial crop. India is the largest cotton growing country with an area of 117.27 lakh hectares and production of 398 lakh bales of cotton lint with an average productivity of 577 kg per ha (Cotton Advisory Board, 2014). Karnataka produced around 23 lakh bales of cotton lint from an area of 5.94 lakh hectares with a productivity of 658 kg per ha (Cotton Advisory Board, 2014).

Genetic diversity of parental lines is a good indicator of the performance of the progeny. Success through hybridization and subsequent selection depends primarily on the selection of the parents having genetic variability for various agronomic traits (Murty and Arunachalam, 1966). Description of a line or variety based upon a trait that reflect genetic variation, can be used to measure the genetic diversity and can therefore, be used to monitor and promote efficient conservation and utilization of genetic diversity. Traits used for genetic diversity analysis in cotton

include morphological characters and agronomical performance and other advance procedure/ methods (Brown, 1991).

In any successful variety improvement programme species, genetic distance estimates among genotypes are helpful in the selecting the genotype combinations for segregating population so as to maintain genetic diversity in breeding programme. These estimates in turn, become the estimates for availability for alternate alleles for desirable traits, which is the basis for long term selection grains. Crosses between genetically divergent parents are expected to have a large genetic varience among the progenies than crosses between closely related parents (Messmer *et al.,* 1993) increasing the opportunity for selecting rare progenies that may be superior.

Genetic diversity is of considerable practical interest in any crop improvement programme. Precise information on the nature and degree of genetic divergence would help the plant breeder in choosing the right type of parents for different breeding programmes. Therefore, the present investigation was undertaken to study the nature and magnitude of genetic divergence in 190 recombinant genotypes of upland cotton derived from interspecific crosses. Individual lines are superior for seed cotton yield and fiber traits.

MATERIAL AND METHODS

One ninety derivatives of F_9 generation of cross between DS-28 and SBYF-425 were conducted under unprotected condition during *Kharif*, 2012-13 at Agricultural Research Station, Dharwad Farm, University of Agricultural Sciences Dharwad. Sowing was done by hand dibbling in rows of each 6m length with spacing of 90cm between rows and 20cm between plants within a row. Sowing was done in Augmented Design-II (Extended form of RBD) with 20 blocks to obtain minimum of 12 error degrees of freedom and six checks repeated in each block. Data were analyzed using Windostat software version 9.1. A recommended package of practice was followed to raise healthy crop under assured rain fed conditions.

Observations on yield and yield related traits *viz.*, plant height (cm), number of monopodia, number of sympodia, boll number, boll weight (g), seed cotton yield (kg/ha), ginning outturn (%), lint index (g), seed index (g) and fibre traits *viz.*, 2.5% span length (mm), fibre strength (g/tex), micronaire value (µg/in) and uniformity ratio (%) were recorded on randomly chosen plants in each blocks. The genetic divergence was worked out by using Mahalanobis D^2 statistics as described by Rao (1952). On the basis of D^2 values the genotypes were grouped into different clusters by employing Tocher's method as out lined by Rao (1952).

RESULTS AND DISCUSSIONS

Mean performance of lines derived from cross between *G. hirsutum* and *G. barbadense.* The lines derived from cross between *G. hirsutum* var. DS-28 and *G. barbadense* var. SBYF-425 were used in the present study. The aim of cross was to combine high yielding potentiality of *G. hirsutum* and high fibre length (>30mm) and fibre strength (>22g/tex) characters from *G. barbadense*. All one ninety recombinant inbred lines (for yield and yield related traits) and 85 (fibre quality) selected at F_9 were used for estimation of genetic diversity. The mean values of different characters were utilized for working out genetic distance between pairs of recombinant inbred lines.

All the 190 recombinant inbred lines were grouped in three clusters based on the diversity for yield and yield contributing traits. Among the three clusters, cluster I was the largest with 171 recombinant inbred lines followed by cluster II and III which had 18 and 1 recombinant inbred lines, respectively (Table 1 & Figure 1). The mean values of 85 RILs for fibre traits were also utilized for working out genetic distance between pairs of recombinant inbred lines. All the

85 recombinant inbred lines were grouped in ten clusters. Among the ten clusters, cluster II was the largest with 41 recombinant inbred lines followed by cluster VI and I with 16 and 13 recombinant inbred lines respectively and cluster IV and V had two recombinant inbred lines, while clusters VII, VIII, IX and X were solitary cluster with single recombinant inbred line (Table 4 & Figure 2).

The contribution of various characters towards the expression of genetic divergence based on morphological, yield and yield contributing traits indicated that the seed cotton yield per ha was the largest contributor with 92.19 per cent towards divergence followed by plant height (6.81 %), ginning outturn percentage (0.71%) and number of bolls per plant (0.25%). Higher contribution of seed cotton yield to total divergence was also reported by Sandhu and Boparai (1977), Amudha *et al.* (1997) and Pushpam *et al.* (2004) in upland cotton (Table 2). The 2.5% span length was the largest contributor with 45.85 per cent towards divergence followed by uniformity ratio (42.44%), fibre strength (11.29%) and micronaire value (0.42%) (Table 5). Sambamurthy *et al.* (1995) and Gururajan and Manickam (2002) and Ali *et al.* (2009) in their experiment on diversity studies for fibre traits concluded that 2.5% span length contributes more to the total divergence. The above results imply that in order to select genetically diverse genotypes, the material should be screened for the important traits like seed cotton yield, plant height, ginning outturn percentage, number of bolls per plant, 2.5% span length, uniformity ratio and fibre strength.

Analysis of cluster means revealed the relative contribution of different traits to the total divergence by the different clusters. Based on range of means, it is possible to know the characters influencing divergence. It helps to identify clusters having different levels of variability for different characters, based on final ranks it is possible to identify clusters having higher and lesser diversity for more number of characteristics. Utilization of low ranked clusters in breeding programme is expected to yield desirable lines in advanced generation of selection.

CONCLUSIONS

In the present investigation based on morphological and yield contributing traits, it was observed that genotypes grouped under Cluster III ranked first by having seven character (1-2 scores) at desirable direction followed by genotypes under cluster II with eight character (1-2 scores) and Genotypes grouped under cluster I (third rank) recorded six characters in negative direction (3 scores) (Table 3). Therefore selection of genotypes falling in cluster III and II would be useful to generate desirable genetic resource on crossing between the germplasm lines present in the clusters. For fibre traits, genotypes were grouped under cluster IX and X ranked first by having two and three character respectively (1-5 scores) at desirable direction followed by genotypes under cluster II and VIII with four and two character respectively (1-5 scores) and cluster III with two character. Genotypes grouped under cluster VII (8^{th}, last rank) recorded three characters in negative direction (6-10 scores). Germplasm present in X cluster (I cluster rank based on cluster mean) poses three characters like 2.5% span length(2rd rank), uniformity ratio (3rd rank) and fibre strength (2^{nd} rank) on desirable direction, so these germplasm lines may be more useful in breeding for fibre quality improvement (Table 6). Therefore, selection of genotypes falling in cluster X, IX, VIII and II would be useful to generate desirable genetic resource on crossing between the germplasm lines present in the clusters. Based on D^2 values, 190 RILs were grouped into three clusters indicating presence of low diversity among the RILs.

REFERENCES

1. *Ali Mabub and Lewis C. F., 2009, Effects of reciprocal crossing on cytological and morphological features of interspecific hybrids of G. hirsutum x G. barbadense. Crop Sci., **2(1)**: 20-22.*

2. *Amudha, K., Raveendran, T. S and Krishnadoss, D., 1997, Genetic diversity in coloured linted cotton varieties. Madras Agric. J., **84**: 334-337.*

3. *Anonymous, 2012, All India Coordinated Cotton Improvement Project (AICCIP). Annu. Rep., 2011-12.*

4. *Brown, J.S., 1991, Principal component and cluster analysis in cotton variability across the US cotton belt – Crop Sci., **31:** 915-922.*

5. *Gururajan, K. N and Manickam, S., 2002, Genetic divergence in Egyptian cotton (G. barbadense L.). J. Indian Soc. Cotton Improv., **27**(2): 86-89.*

6. *Messmer, M. M., Melchinger, A. E., Herrmann, R. G and Jurgen, B., 1993, Relationship among early Europian maize inbreds: II comparison of pedigree RFLP. Crop Sci., **33:** 944-950.*

7. *Murty, B.R and Arunachalam, V., 1966, the nature of genetics divergence in relation to breeding system in some crop plants. Indian J. Genet., **26:** 188-198.*

8. *Pushpam, R., Raveendran, T. S., Devasena, N. and Ravikesavan, R., 2004, Studies on genetic diversity in upland cotton (Gossypium hirsutum). J. Indian Soc. Cotton Improv., **29**(2): 135-143.*

9. *Rao, C. R., 1952, Advanced Statistics Methods in Biometry, John Wiley, New York, pp. 357-369.*

10. *Sambamurthy, J. S. V., Mohan Reddy, D and Reddy, K. H. G., 1995, Studies on the nature of genetic divergence in upland cotton (G. hirsutum L.). Ann. Agric. Res., **16**(3): 307-310.*

11. *Sandhu, B. S and Boparai, M. S., 1997, Genetic divergence in Gossypium arboreum L. Indian J. Gene. Plant Breed. **57**(4): 461-465.*

APPENDIXES

Table 1: Cluster-Wise Distribution of Recombinant Inbred Lines

Cluster	No. of Genotypes	Recombinant inbred lines
I	171	DCHRIL 1, DCHRIL 2, DCHRIL 4, DCHRIL 5, DCHRIL 6, DCHRIL 8, DCHRIL 9, DCHRIL 10, DCHRIL 11, DCHRIL 13, DCHRIL 14, DCHRIL 15, DCHRIL 16, DCHRIL 19, DCHRIL 20, DCHRIL 21, DCHRIL 22, DCHRIL 26, DCHRIL 27, DCHRIL 28, DCHRIL 29, DCHRIL 30, DCHRIL 32, DCHRIL 33, DCHRIL 34, DCHRIL 36, DCHRIL 37, DCHRIL 38, DCHRIL 39, DCHRIL 40, DCHRIL 41, DCHRIL 42, DCHRIL 45, DCHRIL 46, DCHRIL 47, DCHRIL 49, DCHRIL 50, DCHRIL 51, DCHRIL 52, DCHRIL 53, DCHRIL 55, DCHRIL 56, DCHRIL 57, DCHRIL 59, DCHRIL 60, DCHRIL 62, DCHRIL 63, DCHRIL 64, DCHRIL 65, DCHRIL 66, DCHRIL 67, DCHRIL 69, DCHRIL 70, DCHRIL 72, DCHRIL 73, DCHRIL 74, DCHRIL 75, DCHRIL 76, DCHRIL 77, DCHRIL 79, DCHRIL 80, DCHRIL 81, DCHRIL 82, DCHRIL 84, DCHRIL 85, DCHRIL 87, DCHRIL 89, DCHRIL 91, DCHRIL 92, DCHRIL 95, DCHRIL 96, DCHRIL 97, DCHRIL 98, DCHRIL 99, DCHRIL 100, DCHRIL 101, DCHRIL 103, DCHRIL 104, DCHRIL 106, DCHRIL 108, DCHRIL 109, DCHRIL 111, DCHRIL 113, DCHRIL 114, DCHRIL 116, DCHRIL 117, DCHRIL 118, DCHRIL 119, DCHRIL 120, DCHRIL 121, DCHRIL 122, DCHRIL 123, DCHRIL 124, DCHRIL 125, DCHRIL 126, DCHRIL 127, DCHRIL 129, DCHRIL 131, DCHRIL 132, DCHRIL 133, DCHRIL 134, DCHRIL 135, DCHRIL 136, DCHRIL 137, DCHRIL 138, DCHRIL 141, DCHRIL 142, DCHRIL 144, DCHRIL 145, DCHRIL 146, DCHRIL 149, DCHRIL 151, DCHRIL 152, DCHRIL 154, DCHRIL 155, DCHRIL 156, DCHRIL 157, DCHRIL 160, DCHRIL 164, DCHRIL 165, DCHRIL 166, DCHRIL 167, DCHRIL 170, DCHRIL 171, DCHRIL 173, DCHRIL 174, DCHRIL 176, DCHRIL 177, DCHRIL 183, DCHRIL 184, DCHRIL 185, DCHRIL 186, DCHRIL 187, DCHRIL 188, DCHRIL 189, DCHRIL 190, DCHRIL 191, DCHRIL 192, DCHRIL 193, DCHRIL 194, DCHRIL 195, DCHRIL 196, DCHRIL 197, DCHRIL 198, DCHRIL 199, DCHRIL 200, DCHRIL 202, DCHRIL 203, DCHRIL 204, DCHRIL 206, DCHRIL 207, DCHRIL 208, DCHRIL 210, DCHRIL 211, DCHRIL 212, DCHRIL 219, DCHRIL 220, DCHRIL 222, DCHRIL 223, DCHRIL 224, DCHRIL 225, DCHRIL 228, DCHRIL 230, DCHRIL 232, DCHRIL 234, DCHRIL 235, DCHRIL 237, DCHRIL 238, DCHRIL 239, DCHRIL 240, DCHRIL 241, DCHRIL 242, DCHRIL 245, DCHRIL 251, DCHRIL 252, DCHRIL 254
II	18	DCHRIL 110, DCHRIL 153, DCHRIL 68, DCHRIL 140, DCHRIL 159, DCHRIL 147, DCHRIL 150, DCHRIL 43, DCHRIL 141, DCHRIL 168, DCHRIL 58, DCHRIL 178, DCHRIL 126, DCHRIL 179, DCHRIL 163, DCHRIL 44, DCHRIL 180, DCHRIL 169
III	1	DCHRIL 158

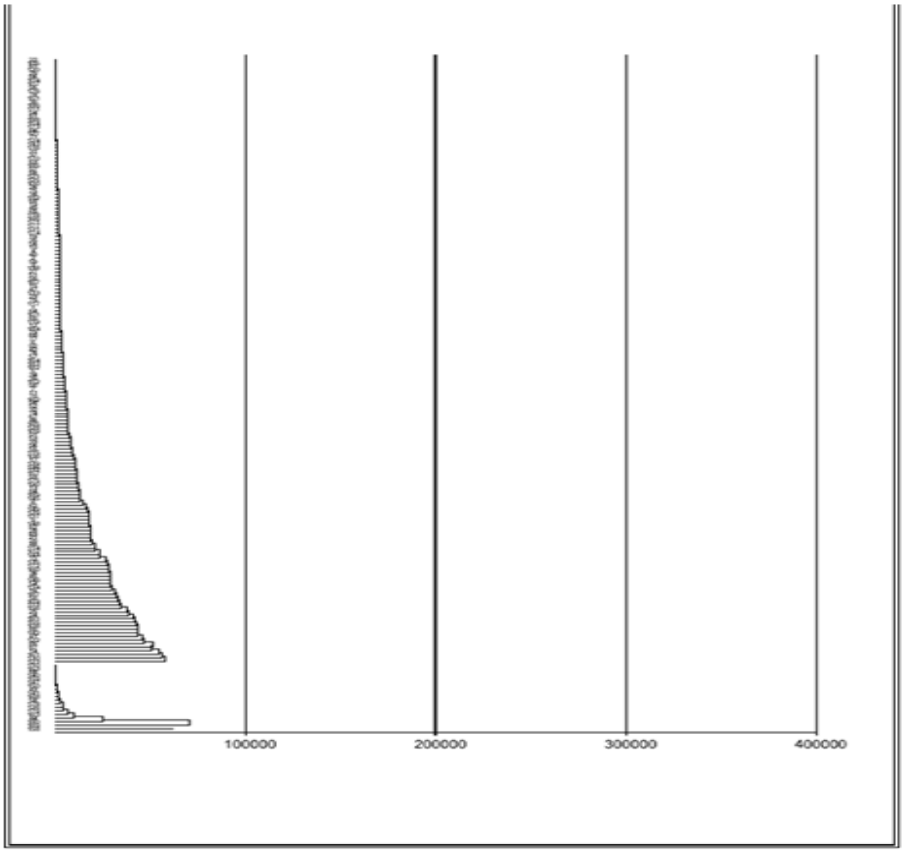

Figure 1: Dendrogram Depicting Genetic Diversity for RILs

Table 2: Contribution of Different Yield and Yield Related Characters Towards Divergence in Recombinant Inbred Lines

Sl. No.	Characters	Per Cent Contribution
1	Seed cotton yield/ha (kg)	92.19
2	Plant height (cm)	6.81
3	Ginning outturn (%)	0.71
4	No. of bolls/ plant	0.04
5	No. of sympodia /plant	0.25

Table 3: The Cluster-Wise Mean Values of Recombinant Inbred Lines for Yield and Yield Related Traits

Cluster	Plant Height (cm)	No. of Monopodia/ Plant	No. of Sympodia/ Plant	No. of Bolls/Plant	Boll Weight (g)	Seed Index (g)	GOT(%)	Lint Index (g)	Seed Cotton Yield per Plant (g)	Seed Cotton Yield kg/ha	Score	Rank
I	69.97 (1)	1.31 (2)	13.62 (1)	3.37 (3)	1.97 (3)	8.87 (3)	30.57 (2)	5.35 (3)	3.22 (3)	179.15 (3)	24	III
II	62.04 (2)	1.58 (1)	11.83 (2)	3.43 (2)	2.45 (2)	10.54 (2)	29.31 (3)	6.06 (2)	9.08 (2)	504.32 (2)	20	II
III	53.20 (3)	1.00 (3)	8.60 (3)	3.60 (1)	2.52 (1)	11.20 (1)	32.60 (1)	7.15 (1)	18.10 (1)	1005.56 (1)	16	I

Values in parenthesis indicates the cluster mean rank

Table 4: Cluster-Wise Distribution of Recombinant Inbred Lines for fibre Traits

Cluster	No. of Genotypes	Recombinant Inbred Lines
I	13	DCHRIL 5, DCHRIL 45, DCHRIL 44, DCHRIL 25, DCHRIL 23, DCHRIL 9, DCHRIL 43, DCHRIL 36, DCHRIL 31, DCHRIL 24, DCHRIL 34, DCHRIL 20, DCHRIL 2
II	41	DCHRIL 53, DCHRIL 72, DCHRIL 42, DCHRIL 28, DCHRIL 30, DCHRIL 68, DCHRIL 17, DCHRIL 18, DCHRIL 67, DCHRIL 52, DCHRIL 81, DCHRIL 39, DCHRIL 22, DCHRIL 11, DCHRIL 65, DCHRIL 19, DCHRIL 14, DCHRIL 61, DCHRIL 1, DCHRIL 6, DCHRIL 10, DCHRIL 58, DCHRIL 50, DCHRIL 47, DCHRIL 3, DCHRIL 74, DCHRIL 60, DCHRIL 37, DCHRIL 8, DCHRIL 48, DCHRIL 56, DCHRIL 29, DCHRIL 64, DCHRIL 12, DCHRIL 76, DCHRIL 77, DCHRIL 21, DCHRIL 15, DCHRIL 51, DCHRIL 71, DCHRIL 83
III	7	DCHRIL 16, DCHRIL 32, DCHRIL 80, DCHRIL 66, DCHRIL 59, DCHRIL 62, DCHRIL 79
IV	2	DCHRIL 13, DCHRIL 85
V	2	DCHRIL 40, DCHRIL 78
VI	16	DCHRIL 4, DCHRIL 33, DCHRIL 54, DCHRIL 49, DCHRIL 55, DCHRIL 12, DCHRIL 73, DCHRIL 41, DCHRIL 63, DCHRIL 7, DCHRIL 26, DCHRIL 57, DCHRIL 84, DCHRIL 27, DCHRIL 75, DCHRIL 69
VII	1	DCHRIL 35
VIII	1	DCHRIL 70
IX	1	DCHRIL 38
X	1	DCHRIL 46

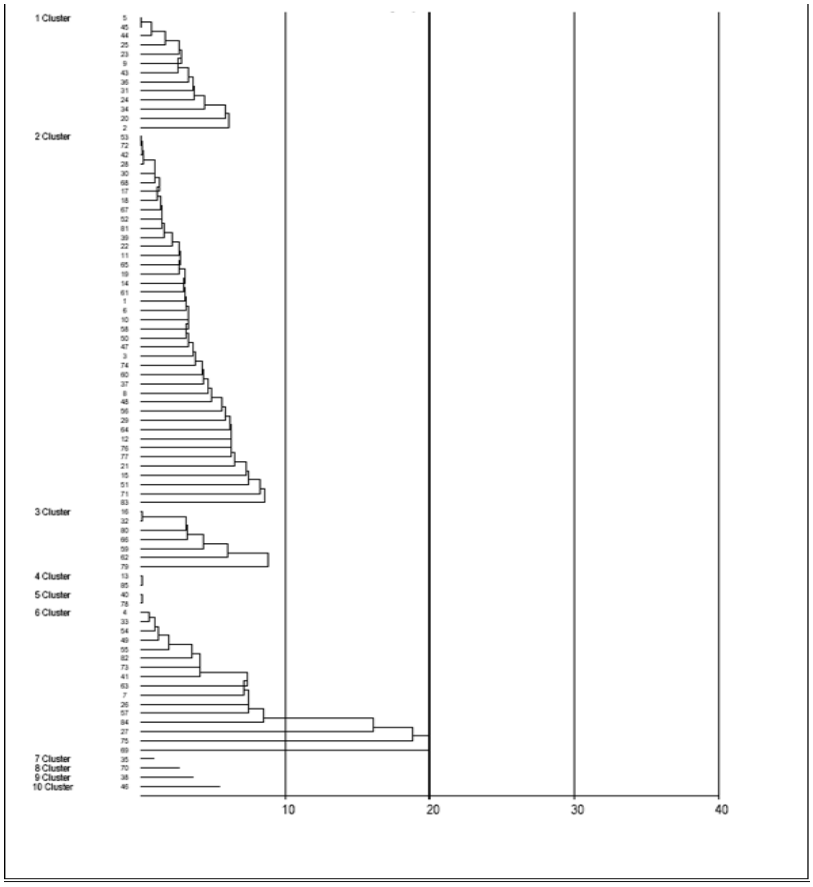

Figure 2: Dendrogram Depicting Genetic Diversity for Fibre Quality Traits

Table 5: Contribution of different fibre Characters towards Divergence in Recombinant Inbred Lines

Sl. No.	Characters	Per Cent Contribution
1	2.5% span length	45.85
2	Uniformity ratio (%)	42.44
3	Fibre strength (g/tex)	11.29
4	Micronaire value (µg/in)	0.42

Table 6: The Cluster-Wise Mean Values of RecombinantInbred Lines for Fibre Traits

Cluster	2.5% Span Length (mm)	Uniformity Ratio (%)	Micronaire (µg/in)	Fibre Strength 3.2mm (g/tex)	Score	Rank
I	22.77 (10)	49.85 (2)	3.32 (6)	18.94 (7)	25	VII
II	26.25 (5)	48.61 (4)	3.37 (5)	20.17 (4)	18	II
III	24.63 (6)	51.57 (1)	3.14 (9)	20.50 (3)	19	III
IV	24.15 (7)	48.50 (5)	3.80 (3)	18.10 (9)	24	VI
V	24.00 (8)	48.50 (5)	3.95 (1)	18.30 (8)	22	V
VI	27.40 (4)	45.50 (8)	3.38 (4)	19.76 (5)	21	IV
VII	23.30 (9)	47.00 (7)	3.90 (2)	17.90 (10)	28	VIII
VIII	28.00 (3)	48.00 (6)	3.20 (8)	23.50 (1)	18	II
IX	30.20 (1)	49.00 (3)	3.30 (7)	19.50 (6)	17	I
X	30.00 (2)	49.00 (3)	3.10 (10)	22.80 (2)	17	I

Values in parenthesis indicates the cluster mean rank